Amendments to the Specification

Please insert the following sentence into the first line of the specification:

--This application is a National Stage of International Application PCT/EP/03/014840, filed December 19, 2003, which claim benefit of EP 02028530.0, filed December 19, 2002, and which claims benefit of EP 03090275.3, filed August 29, 2003.--

Please replace the paragraph at pp. 5 lines 7-15 with the following:

--To date, plants have been described in which the activity of an SSIII protein (Abel et al., 1996, The Plant Journal 10(6), ~~9891-991~~ 981-991; Lloyd et al., 1999, Biochemical Journal 338, 515-521) or the activity of a BEI protein (Kossman et al. 1991, Mol Gen Genet 230, 39-44); Safford et al., 1998, Carbohydrate Polymers 35, 155-168, or the activity of a BEII protein (Jobling et al., 1999, The Plant Journal 18(2): 163-171, or the activity of a BEI and a BEII protein (Schwall et al., 2000, Nature Biotechnology 18, 551-554; WO 96/34968), or the activity of a BEI and an SSIII (WO 00/08184) protein are ~~reduced .~~ reduced.--

Please replace the paragraph at pp. 7 lines 1-21 with the following:

--In this context, the mutation can be generated by using chemical agents or high-energy radiation (for example x-rays, neutron, gamma, UV radiation). Agents which can be employed for generating chemically induced mutations, and the mutations generated thereby by the action of the mutagens in question, are described, for example, by Ehrenberg and Husain, 1981, (Mutation Research 86, 1-113), Müller, 1972 (Biologisches Zentralblatt 91 (1), 31-48). The generation of rice mutants using gamma rays, ethyl methanesulfonate (EMS), N-methyl-N-nitrosurea or sodium azide ~~(NaN3)~~ (NaN_3) is described, for example, in Jauhar and Siddiq (1999, Indian Journal of Genetics, 59 (1), 23-28), in Rao (1977), Cytologica 42, 443-450), Gupta and Sharma (1990, Oryza 27, 217-219) and Satoh and Omura (1981, Japanese Journal of Breeding 31 (3), 316-326). The generation of wheat mutants using NaN_3 or maleic hydrazide is described in Arora et al. (1992 ~~Anals~~ Annals of Biology 8 (1), 65-69). An overview over the generation of

wheat mutants using different types of high-energy radiation and chemical agents is given in Scarascia-Mugnozza et al. (1993, Mutation Breeding Review 10, 1-28). Svec et al. (1998, Cereal Research Communications 26 (4), 291-396) describes the use of N-ethyl-N-nitrosurea for generating mutants in triticale. The use of MMS and gamma radiation for generating millet mutations is described in Shashidhara et al. (1990, Journal of Maharashtra Agriculture Universities 15 (1), 20-23).--

Please replace the paragraph at pp. 12 lines 21-31 with the following:

--SSIII proteins are described, for example, by Marshall et al. ~~(The Plant Cell 8; (1996); 1121-1135)~~ (1996, The Plant Cell 8, 1121-1135), Lie et al. (2000, Plant Physiology 123, 613-624), Abel et al. (The Plant Journal 10(6); (1996); 981-991) and in ~~WO 0066745~~ WO 00/66745. The structure of SSIII proteins frequently shows a sequence of domains. At the N terminus, SSIII proteins have a signal peptide for the transport into plastids. Towards the C terminus, this is followed by an N-terminal region, an SSIII-specific region and a catalytic domain (Li et al., 2000, Plant Physiology 123, 613-624). Further analyses which are based on primary sequence alignments ~~(http://hits.isb-sib.ch/cgi-bin/PFSCAN)~~, revealed that the potato SSIII protein has what is known as a carbohydrate binding domain (CBM). This domain (Pfam motiv cbm 25) comprises the--

Please replace the paragraph at pp. 13 lines 8-27 with the following:

--The term homology, or identity, is understood as meaning the number of agreeing amino acids (identity) with other proteins, expressed in percent. The identity is preferably determined by comparing the Seq ID No. 3 with ~~othen~~ other proteins with the aid of computer programmes. If sequences which are compared with each other are different in length, the identity is to be determined in such a way that the number of amino acids which the short sequences shares with the longer sequence determines the percentage identity. The identity can be determined routinely by means of known computer programmes which are publicly available such as, for example, ClustalW (Thompson et al., Nucleic Acids Research 22 (1994), 4673-4680). ClustalW is made publicly available by Julie Thompson ~~(Thompson@EMBL-Heidelberg.DE)~~ and Toby Gibson

~~(Gibson@EMBL-Heidelberg.DE)~~, European Molecular Biology Laboratory, Meyerhofstrasse 1, D 69117 Heidelberg, Germany. ClustalW can likewise be downloaded from various internet pages, inter alia the IGBMC (Insitut de Génétique et de Biologie Moléculaire et Cellulaire, B.P.163, 67404 Illkirch Cedex, France~~; ftp://ftp-igbmc.u-strasbg.fr/pub/~~) and the EBI (~~ftp://ftp.ebi.ac.uk/pub/software/~~) and all mirrored EBI internet pages (European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK).--

Please replace the paragraph at pp. 14 lines 3-17 with the following:

--One possibility of finding similar sequences is to carry out sequence database researches. Here, one or more sequences are entered as what is known as a query. This query sequence is then compared with sequences present in the selected databases using statistical computer programmes. Such database queries (blast searches) are known to the skilled worker and can be carried out at different suppliers. If, for example, such a database query is carried out at the NCBI (National Center for Biotechnology Information~~, http://www.ncbi.nlm.nih.gov/~~), the standard setting for the respective comparison query should be used. For protein sequences comparisons (blastp), these settings are: Limit entrez = not activated; Filler = low complexity activated; Expect value = 10; word size = 3; Matrix = BLOSUM62; Gap costs: Existence = 11, Extension = 1. The result of such a query is, among other parameters, the degree of identity between the query sequence and the similar sequences found in the databases.--